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Generation means analysis of plant architectural traits and fruit yield in melon

J. E. Zalapa[1], J. E. Staub[1] and J. D. McCreight[2]

[1]Vegetable Crops Unit, Department of Horticulture, US Department of Agriculture, Agricultural Research Service, 1575 Linden Dr., University of Wisconsin, Madison, WI 53706, USA, E-mail: jezalapa@wisc.edu; [2]Agricultural Research Station, US Department of Agriculture, Agricultural Research Service, 1636 East Alisal, Salinas, CA 93905, USA

With 2 tables

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Abstract

Unique architectural phenotypes have the potential for increasing yield in commercial melon (*Cucumis melo* L.). Therefore, a generation means analysis was conducted to investigate the inheritance of architectural traits (days to anthesis, primary branch number, fruit number and weight, and average weight per fruit). Progeny (F_1, F_2, BC_1P_1 and BC_1P_2) from a cross between US Department of Agriculture (USDA) line, USDA 846-1 (P_1) and 'TopMark' (P_2) were evaluated at Arlington (AR) and Hancock (HCK), Wisconsin in 2001. Significant ($P \leq 0.05$) environment effects and genotype × environment interactions (G × E) analyses necessitated analysis by location. Significant differences ($P \leq 0.05$) among parents and generations were observed for all traits, and the two parental lines differed significantly for primary branch number, fruit number and average weight per fruit. Additive gene effects were most important in governing primary branch number and fruit number per plant, while dominance and epistatic genetic effects mainly controlled days to anthesis, fruit weight per plant and average weight per fruit. Narrow-sense heritabilities were 0.62 (AR) for days to anthesis, 0.71 (AR) and 0.76 (HCK) for primary branch number, 0.68 (AR) and 0.70 (HCK) for fruit weight per plant, 0.33 (AR) and 0.45 (HCK) for fruit weight per plant, and 0.06 (AR) and 0.79 (HCK) for average weight per fruit. Estimations of the least number of effective factors for primary branch number were relatively consistent at both AR (approx. 4) and HCK (approx. 2). Results suggest that introgression of yield-related genes from highly branched melon types (e.g. USDA 846-1) into US Western Shipping germplasm may aid in the development of high-yielding cultivars with concentrated fruit set suitable for machine and/or hand-harvesting operations.

Key words: *Cucumis melo* — primary branch number — quantitative inheritance — gene action — epistasis

Melon (*Cucumis melo* L.; $2n = 2 \times = 24$) is an economically important, cross-pollinated, vegetable species, which is subdivided into six cultivar groups: Cantalupensis, Inodorous, Flexuosus, Conomon, Chito-Dudaim and Momordica (Munger and Robinson 1991). In the United States, Group Cantalupensis market types (i.e. Western Shipping and Eastern Market) are most important for commercial production. Arizona, California, Texas, Georgia and Indiana are the primary producers of cantaloupes for US fresh market consumption (NASS 2003). In 2003, US farmers grew almost 37 000 ha (90 000 acres) of cantaloupes for a total production in excess of 1 million tons having a market value of almost 400 million US dollars (NASS 2003).

High yield and uniform fruit shape, size and excellent quality are prerequisites for the release of superior melon varieties. Yield is correlated with several traits including days to anthesis, primary branch number, fruit number and weight per plant and average weight per fruit (Lippert and Hall 1982, Kultur et al. 2001, Abdalla and Aboul-Nasr 2002, Taha et al. 2003). Heterosis for yield and/or its associated components has been reported in melon (Bohn and Davis 1957, Foster 1967, Dhaliwal 1995, Abdalla and Aboul-Nasr 2002, Kubicki 1962, Rosa 1927, Scott 1933, Munger 1942, Lippert and Hall 1982). However, few studies have examined the inheritance of traits affecting yield in this vegetable crop species (Lippert and Legg 1972, Lippert and Hall 1982, Dhaliwal 1995). Lippert and Legg (1972) evaluated the gene action of yield traits in melon, and determined that additive (general combining ability) and non-additive (specific combining ability) variance components were important in the genetic control of yield-associated traits. However, the relative importance of additive, dominant and epistatic contributions was not reported, and other studies that evaluate gene action controlling such traits in melon do not exist.

Generation means analysis (GMA; Mather and Jinks 1982) has been used successfully to study the genetics of melon resistance to vine decline, which is caused by the fungus *Acremonium cucurbitacearum* (Dias et al. 2004). Given the lack of genetic information related to yield components in melon, a GMA study was designed to: (i) determine gene action; (ii) estimate components of variance; (iii) estimate broad- and narrow-sense heritabilities; and (iv) calculate the minimum number of effective factors of several yield components in this crop species. An assessment of these genetic parameters will allow for the development of efficient breeding strategies for melon cultivar improvement.

Materials and Methods

Plant materials: Horticulturally unique germplasm of melon, *Cucumis melo* L., designated CR1 [available at the US Department of Agriculture, Agricultural Research Service (USDA, ARS) melon breeding project, Madison, WI] was used in the production of an inbred line, USDA 846-1 (Staub et al. 2004, Zalapa et al. 2004). This line possesses a unique growth habit similar to CR1, characterized by its extreme 'fractal' or radiant growth habit (Prusinkiewicz and Haran 1989), which is distinct from vining (Rosa 1924), dwarf (Denna 1962, Mohr and Knavel 1966) and birdnest (Paris et al. 1981) melon plant habits. USDA 846-1 is monoecious, highly branched (five to eight primary branches), produces a concentrated fruit-set (two to five fruits near the crown of the plant) and is capable of multiple fruiting cycles at commercial US open-field spacing (0.35 m within row spacing on 2-m centres; 72 600 plants/ha) (Staub et al. 2004, Zalapa et al. 2004). Like CR1, the fractal architecture of USDA 846 is a function of its

internode length (standard size) and comparatively high number of primary, secondary and tertiary branches. USDA 846-1 (P_1) was crossed to 'TopMark' (P_2), which is andromonoecious, possesses between two to four lateral branches, and produces a diffuse, distal fruiting setting habit typical of vining melon types. A single F_1 plant from this initial mating was used as the paternal parent to produce BC_1P_1 ($P_1 \times F_1$) and BC_1P_2 ($P_2 \times F_1$) progeny, and was also self-pollinated to generate F_2 progeny.

Experimental design: Seeds from each of the six generations (i.e. P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2) and a control cultivar, 'Hale's Best Jumbo' (Excel Seeds, Chattanooga, TN, USA) were sown in 72-unit plastic potting trays (T.O. Plastics, Inc., Clearwater, MN, USA) containing Growing Mix No. 2 (Conrad Fafard, Inc., Agawam, MA, USA). Trays were held in a greenhouse at the UW Madison, WI during the spring of 2001, watered once a day, and fertilized (N : P : K = 20 : 20 : 20) twice before transplanting. Three-week-old seedlings were 'hardened-off' outdoors for 3 days, fertilized with starter fertilizer (N : P : K = 10 : 24 : 8) and transplanted to rows covered with 1-mm black plastic at the University of Wisconsin experimental farms at Arlington (AR) and Hancock (HCK), WI. To obtain individual plant measurements, transplants were spaced at 0.70 m within rows on 2 m centres (36 30 plants/ha), and standard cultivation practices were followed according to UWEX (2001) for Hancock's Planefield loamy sand (Typic Udipsamment) and Arlington's Plano silt loam (Typic Argiudoll) soil types.

The experimental design was a randomized complete block design (RCBD) consisting of three blocks with 10 plants per plot. Within each block the segregating generations (i.e. BC_1 and F_2) were replicated three and five times, respectively. 'Hale's Best Jumbo' was used to provide a benchmark for maturation rate and harvest timing.

Data collection: Days to anthesis was taken as the number of days from transplanting to the time one fully expanded flower was present per individual plant. The number of primary branches for each plant was counted 30 days after transplant to include all branches of more than 12.5 cm in length below the fourth node. Fruit number and fruit weight (kg) were collected per plant using all fruits of at least 7.5 cm in diameter at 80 days after transplanting. The average weight per fruit was calculated for each plant by dividing the total weight per plant by the total number of fruit per plant. Data on days to anthesis for staminate flowers were collected only at AR, while data on primary branch number, and fruit number and weight per plant were collected at both AR and HCK.

Statistical and genetic analyses: Initially, data were combined to determine location and genotype × location effects. As these effects were significant for all traits examined, the data from each location were analysed separately. Analyses of variances were performed using PROC MIXED (SAS Institute 1999), where locations and generations were treated as fixed effects and blocks were considered as random effects. Phenotypic correlations (r; n = 6) were calculated by location using PROC CORR (SAS Institute 1999).

Analyses of generations by GMA were conducted using a joint scaling test based on an additive–dominance model (Cavalli 1952, Mather and Jinks; JNTSCALE software, Ng 1990), non-weighted scaling test method based on a six-parameter model (Jinks and Jones 1958; JNTSCALE software, Ng 1990) and using sequential parameter model fitting (Kearsey and Pooni 1996; SAS 1990). The average gene effects expectations of the six basic generations are given as proposed by Mather and Jinks (1982).

Phenotypic, genotypic and environmental variances were estimated for each population using the model of Mather and Jinks (1982). The standard error of each parameter was calculated as proposed by Lynch and Walsh (1998). Broad- (h^2_B) and narrow- (h^2_N) sense heritabilities, and their standard errors were calculated as proposed by Becker (1992) and Hallauer and Miranda (1988). Equations by Castle (1921) and Wright (1968) were utilized to estimate the minimum number of effective factors (n) operating in each location.

Results

Generation means analyses

Significant ($P \leq 0.05$) mean differences were detected between the two parental lines for all traits, at both AR and HCK, except for days to anthesis and fruit weight per plant (Table 1). Parent rankings were reversed depending on the growing location for fruit number and fruit weight per plant and average weight per fruit. Although significant differences ($P \leq 0.05$) were not detected between the parental lines at AR for days to anthesis, P_1 flowered earlier than P_2 and 'Hale's Best Jumbo' (33.6, 34.8 and 35.2 days, respectively). Similarly, P_1 consistently possessed more primary branches (approx. 6.7) at both locations than either P_2 (approx. 4.0) or 'Hale's Best Jumbo' (approx. 4.3). Individual BC_1P_1, BC_1P_2 and F_2 progeny were observed that reached or transgressed the phenotypic extremes of either parent for most traits and locations.

For most traits, F_1 generation means were higher than the mid-parent value, and at AR the mean of the F_1 surpassed the mean of the high parent for fruit number per plant, weight per plant and days to anthesis (Table 1). The F_1 generation was intermediate to parental lines for primary branch number at both AR (5.7) and HCK (5.6), and performed equal to/or better than both parents for fruit number per plant (5.9, AR and 1.7, HCK), fruit weight per plant (6.2 kg, AR and 2.4 kg, HCK) and average weight per fruit (1.1 kg, AR and 1.5 kg, HCK). BC_1P_1 and BC_1P_2 progeny resembled their respective recurrent parent with respect to growth habit and fruiting characteristics, and F_2 individuals varied dramatically for the yield-related characteristics examined.

Trait correlations

Phenotypic correlations between fruit number and weight per plant were positive and significant ($P \leq 0.01$) at both locations [$r = 0.63$ (AR) and $r = 0.67$ (HCK)]. Significant ($P \leq 0.01$) negative correlations between fruit number per plant and average weight per fruit were detected at both locations [$r = -0.58$ (AR) and $r = -0.58$ (HCK)]. Significant correlations between fruit number per plant and primary branch number and fruit weight per plant and primary branch number were not detected at AR. However, at HCK, primary branch was positively correlated ($P \leq 0.01$) with both fruit number per plant ($r = 0.30$) and fruit weight per plant ($r = 0.22$).

Gene action

Data over locations for all traits did not adequately fit a simple additive–dominance model (three-parameter model) (data not presented; Zalapa 2005). The non-weighted scaling test approach identified significant additive, dominance and non-allelic interactions for all traits. Sequential model fitting using a six-parameter model (i.e. additive, dominance and interactions) identified best-fit models with significant non-allelic interactions for all traits, except primary lateral branching where additive effects predominated in both locations. Although most best-fit models contained non-allelic parameters, some traits were conditioned mainly by additive and/or

Table 1: Least square means (lsmeans), standard errors ($\bar{x} \pm$ SE) and number of plants (n) of yield components in melon (*Cucumis melo* L.) lines USDA 846-1 (P_1) and 'TopMark' (P_2), their progeny (F_1, F_2, BC_1P_1 and BC_1P_2) and 'Hale's Best Jumbo' grown at two Wisconsin locations

	Arlington, WI 2001									Hancock, WI 2001								
	Primary branch number		Fruit number per plant		Fruit weight per plant (kg)		Average weight per fruit (kg)		Days to anthesis[1]	Primary branch number		Fruit number per plant		Fruit weight per plant (kg)		Average weight per fruit (kg)		
Generation	n	$\bar{x} \pm$ SE	n	$\bar{x} \pm$ SE	n	$\bar{x} \pm$ SE	n	$\bar{x} \pm$ SE	n $\bar{x} \pm$ SE	n	$\bar{x} \pm$ SE	n	$\bar{x} \pm$ SE	n	$\bar{x} \pm$ SE	n	$\bar{x} \pm$ SE	n $\bar{x} \pm$ SE
USDA 846-1 (P_1)	30	6.70 a[2] ± 0.23	30	3.80 e ± 0.27	30	4.35 d ± 0.34	30	1.18 b ± 0.05	30 33.63 a ± 0.69	30	6.77 a ± 0.21	30	2.17 a ± 0.24	30	2.45 bc ± 0.21	30	1.33 c ± 0.13
'TopMark' (P_2)	30	3.93 d ± 0.20	29	5.06 abc ± 0.39	29	4.73 cd ± 0.34	29	1.01 c ± 0.06	30 34.83 ab ± 0.54	30	4.37 d ± 0.16	30	1.23 b ± 0.20	30	2.08 c ± 0.21	30	1.80 ab ± 0.11
F_1	30	5.73 b ± 0.25	25	5.88 a ± 0.40	25	6.21 ab ± 0.45	25	1.10 bc ± 0.06	30 33.43 a ± 0.70	30	5.63 b ± 0.22	29	1.72 a ± 0.25	27	2.44 bc ± 0.28	27	1.54 bc ± 0.12
BC_1P_1	90	5.82 b ± 0.19	86	4.07 de ± 0.24	86	5.02 c ± 0.29	86	1.37 a ± 0.07	90 33.58 a ± 0.44	85	5.89 b ± 0.15	85	1.77 a ± 0.20	73	3.07 a ± 0.23	73	1.88 a ± 0.10
BC_1P_2	88	4.82 c ± 0.19	85	4.79 bdc ± 0.24	85	6.63 a ± 0.33	85	1.47 a ± 0.05	88 35.60 b ± 0.53	90	5.07 c ± 0.14	79	1.38 b ± 0.19	71	2.43 bc ± 0.21	71	1.90 a ± 0.11
F_2	147	5.46 b ± 0.19	141	4.61 bdc ± 0.24	141	5.42 bc ± 0.31	141	1.30 ab ± 0.05	147 34.99 b ± 0.48	138	5.69 b ± 0.15	136	1.73 a ± 0.19	116	2.79 ab ± 0.21	116	1.81 ab ± 0.11
'Hale's Best'	30	4.20 d ± 0.21	30	4.13 cde ± 0.37	30	5.36 bc ± 0.43	30	1.39 a ± 0.08	30 35.20 b ± 1.34	30	4.53 d ± 0.15	30	1.87 a ± 0.23	26	2.94 ab ± 0.23	26	1.71 ab ± 0.15
Location	445	5.24	426	4.62	426	5.39	426	1.26	445 34.47	433	5.42	419	1.70	373	2.60	373	1.71	

[1]Days to anthesis data was collected only at Arlington.
[2]Means in the same column with the same letter are not significantly different according to pairwise *t* test comparison at $P \leq 0.05$.

dominance effects. Epistatic interactions were most important in explaining variation associated with days to anthesis and average weight per fruit. The non-weighted scaling and sequential parameter model fitting test results agreed with respect to the relative importance of gene action for all traits examined.

Variance components

Variance component estimates (i.e. σ^2_A, σ^2_D, $V_{A \times D}$, σ^2_G, σ^2_P, $\sigma^2_{P'}$ and σ^2_E) are presented in Table 2. Negative estimates were assumed to be zero (Robinson et al. 1955), but are reported herein as recommended by Dudley and Moll (1969) and Hallauer and Miranda (1988) for historical import. Variance component estimates varied considerably across locations. The magnitude of the variance estimates for primary branch number and average weight per fruit were higher at HCK than at AR. In contrast, fruit number and weight per plant variance estimates obtained at AR were higher than at HCK. The additive genetic variance estimates for days to anthesis, primary branch number and fruit number per plant were positive while their dominance variance estimates were negative. Conversely, the magnitude of additive genetic variance was comparatively smaller than the dominance variance for fruit weight per plant and average weight per fruit at AR, whereas the opposite was the case in HCK. The environmental component of the variance was lower than genetic variance component for all traits in each location.

Heritability and factor number estimates

Broad-sense heritabilities were relatively high for all traits and ranged from 0.64 to 1.00 (Table 2). Narrow-sense heritabilities were 0.62 for days to anthesis (AR), 0.71 and 0.76 (AR and HCK respectively) for primary branch number, 0.68 (AR) and 0.70 (HCK) for fruit number per plant, 0.33 (AR) and 0.45 (HCK) for fruit weight per plant and 0.06 (AR) and 0.79 (HCK) for average weight per fruit. Minimum factor number estimates were negative for all traits, except primary lateral branch number where they were relatively consistent, but differed across locations (AR, approx. 4 and HCK, approx. 2).

Discussion

The number of primary branches in all generations remained comparatively constant at both Arlington (AR) and Hancock (HCK). Similar results were reported for lateral branch number in cucumber (*Cucumis sativus* L.), where environmental effects and $G \times E$ interactions played a minor role in determining branching patterns of diverse genotypes (Serquen et al. 1997a, Fazio 2001). Likewise, Kultur et al. (2001) reported that in melon environmental effects (e.g. growing location and planting density) and concomitant $G \times E$ interactions do not greatly influence branching habit in vining and birdnest genotypes.

Significant positive correlations between primary branch number and yield traits were detected at HCK (Table 2). These results are consistent with those of Taha et al. (2003) who reported positive associations between primary branch number and total yield ($r = 0.82$). Therefore, it may be possible to identify and select extreme fractal melon genotypes with improved (i.e. high yielding) and concentrated early yield from

Table 2: Genetic and environmental components of variances, heritabilities and their standard errors of yield components in melon (*Cucumis melo* L.) lines USDA 846-1 (P_1) and 'TopMark' (P_2) and their progeny (F_1, F_2, BC_1P_1 and BC_1P_2) grown at two Wisconsin locations

	Arlington, WI 2001					Hancock, WI 2001				
Genetic parameter[1]	Primary branch Number	Fruit number per plant	Fruit weight per plant (kg)	Average weight Per fruit (kg)	Days to anthesis[2]	Primary branch number	Fruit number Per plant	Fruit weight per plant (kg)	Average weight per fruit (kg)
σ^2_A	1.92 ± 1.08	6.39 ± 1.34	3.60 ± 1.27	0.04 ± 0.08	14.17 ± 2.35	3.07 ± 1.10	1.74 ± 1.07	1.84 ± 1.10	0.94 ± 0.11
σ^2_D	−2.75 ± 1.22	−8.64 ± 2.23	5.08 ± 1.45	0.52 ± 0.10	−18.98 ± 10.68	−3.94 ± 1.29	−2.72 ± 1.20	1.47 ± 1.15	0.06 ± 0.14
$V_{A\times D}$	0.05 ± 1.02	−0.13 ± 1.07	−1.74 ± 1.15	0.15 ± 0.05	−7.18 ± 1.25	0.04 ± 1.02	0.36 ± 1.02	0.63 ± 1.04	−0.11 ± 0.05
σ^2_G	1.92 ± 1.08	6.39 ± 1.34	8.68 ± 1.85	0.56 ± 0.18	14.17 ± 2.35	3.07 ± 1.10	1.74 ± 1.07	3.30 ± 1.28	1.00 ± 0.25
σ^2_E	0.78 ± 0.23	2.96 ± 0.40	2.34 ± 1.11	0.07 ± 0.19	8.69 ± 2.66	0.94 ± 0.24	0.75 ± 0.22	0.77 ± 0.22	0.19 ± 0.20
σ^2_P	2.70 ± 1.11	9.35 ± 1.52	11.02 ± 2.05	0.63 ± 0.38	22.86 ± 3.42	4.02 ± 1.15	2.49 ± 1.10	4.07 ± 1.32	1.20 ± 0.45
$\sigma^2_{\bar{P}}$	2.11 ± 1.04	7.99 ± 1.16	6.14 ± 1.12	0.43 ± 0.05	22.06 ± 1.50	2.99 ± 1.06	1.88 ± 1.03	2.57 ± 1.05	0.97 ± 0.10
h^2_B	0.91 ± 0.66	0.80 ± 0.32	0.79 ± 0.27	0.89 ± 1.19	0.64 ± 0.17	1.00 ± 0.59	0.93 ± 0.70	0.81 ± 0.45	0.84 ± 0.84
h^2_N	0.71 ± 0.51	0.68 ± 0.27	0.33 ± 0.17	0.06 ± 0.32	0.62 ± 0.16	0.76 ± 0.44	0.70 ± 0.53	0.45 ± 0.33	0.79 ± 0.81

[1] σ^2_A, σ^2_D, $V_{A\times D}$, σ^2_G, σ^2_P, $\sigma^2_{\bar{P}}$, σ^2_E, h^2_B and h^2_N are the additive genetic variance, dominance genetic variance, additive genetic component of variance × dominance genetic component of variance interaction, genetic variance, phenotypic variance = $\sigma^2_A + \sigma^2_D + \sigma^2_E$, phenotypic variance = $2\sigma^2_{F2}$, environmental variance, broad-sense heritability and narrow-sense heritability, respectively.

[2] Days to anthesis (from sowing) data was only collected at Arlington.

the populations developed herein (Staub et al. 2004, Zalapa et al. 2004).

Environmental conditions and G × E interactions can dramatically affect melon fruit development (Davis and Meinert 1965, Kultur et al. 2001). The productivity ranking of the genotypes examined herein varied between the two locations for these traits (Table 1). Such inconsistencies in yield performance between locations and among genotypes can be explained, in part, by differences in source–sink relations due to differences in biomass accumulation as evidenced by vine length and leaf area (Rosa 1924, Hughes et al. 1983). In fact, vine length and leaf area were up to approx. two × times higher in AR than in HCK, and fractal were more vigorous than vining genotypes at both locations (as defined visually by vegetative growth differences and yield data). Thus, fractal genotypes grown at AR and/or HCK likely possessed higher photosynthetic capacity which in turn allowed them to support a higher concentrated yield per plant (i.e. fruit number and weight). For traits such as primary branch number which are conditioned by relatively few (two to four) additive genetic factors, selection can be conducted irrespective of growing environment. These observations are important as selection, for most of the traits examined, must be location dependent.

Fractal types (high branching) produced higher basal-concentrated yield per plant than vining types (low branching) at both AR and HCK (Table 1). However, some vining genotypes (e.g. 'TopMark') grown at AR produced numerous distally set fruit in a secondary fruiting cycle. Fruit development in these genotypes began late in the season (middle of August) and thus these immature fruit would not likely contribute to marketable yield under Wisconsin growing conditions. The observed fruit size differences between locations and among genotypes might have been predicted as fruit number per plant is negatively correlated with average weight per fruit. These results suggest that breeding strategies to increase fruit number per plant and fruit weight per plant while maintaining commercially acceptable average weight per fruit in melon will likely be complicated by contrasting trait correlations and G × E interactions.

The comparatively high heritabilities and/or the consistency of estimates between locations (AR and HCK) for primary branch number and fruit number per plant in this population suggests that these traits are likely amendable to genetic manipulation. The previously unreported primary branch number narrow-sense heritability estimates presented herein are comparable with those for lateral branch number in cucumber (Serquen et al. 1997a). Likewise, the narrow-sense heritability estimates for fruit weight per plant are consistent with the estimates provided Lippert and Hall (1982). In contrast, narrow-sense heritabilities estimates for fruit number per plant and average weight per fruit are not consistent with the estimates reported by Lippert and Hall (1982); $h^2_N = 0.12$ and 0.52, respectively). These disparities are likely due to the use of differing plant architectural types (i.e. extreme fractal, vining and dwarf types, respectively), and/or the methods used for the analyses (i.e. GMA and parent–offspring regression). As dominance, epistasis and G × E interaction may have biased heritability estimates presented herein, more sophisticated mating designs (e.g. F_3 families) should be employed for providing such genetic parameters in extreme fractal melon germplasm.

A simplistic additive–dominance model did not adequately explain the observed variation for any of the traits examined herein, and is evidence for the presence of digenic or higher-order epistatic interactions. This result is supported by quantitative trait loci (QTL) mapping analyses where epistatic interactions were detected during two-dimensional genome analyses (Zalapa et al. 2006). Most of the traits examined exhibited the combined influence of substantial dominance and epistatic effects except for primary branch number and fruit number per plant, which were mainly controlled by additive factors (two to four). These results are supported by QTL analyses (e.g. lateral branching four QTL, LOD > 3.0; $R^2 = 0.51$; Zalapa et al. 2006) and are consistent with Lippert and Legg (1972) who reported that, in addition to general combining ability, specific combing ability was important in the expression of yield and maturity traits in Group Cantalupensis melons. Given the importance of additive effects controlling primary branch number and fruit number per plant, selection for highly branched genotypes with the ability to support basal-concentrated fruit set should be possible in this population. The development of early flowering genotypes possessing desirable fruit weight characteristics (i.e. high fruit weight per plant and average weight per fruit), however, will likely be complicated by inherent dominance and epistatic effects.

Gene action and empirical estimates of genetic parameters governing trait expression have been useful in developing breeding strategies for incorporating genes for high lateral branching in cucumber (Serquen et al. 1997b, Fazio et al. 2003a) in the deployment of marker-assisted selection (MAS) for altering plant architecture (Fazio et al. 2003b, Fan et al. 2006). Increasing lateral branch number and altering the fruit setting habit of melon can provide for the development of early fruiting (i.e. concentrated fruit set), high yielding genotypes (Kultur et al. 2001). The alignment of desirable alleles conditioning such complex traits in melon could be enhanced by the identification of marker–trait associations for their subsequent use in MAS. To this end we have identified 34 QTL (LOD > 3; for primary branch number, fruit number and 10, 9, 5 and 3 for 7, fruit weight, average fruit weight and % mature fruit, respectively) and their associated epistatic interactions for the yield components examined herein using F_6-derived recombinant inbred lines (Zalapa et al. 2006). As these QTL explain a considerable amount of the phenotypic variation ($R^2 = 40$–97%) and their epistatic interactions are now known (empirical; Tables 1 and 2 and QTL analysis ;Zalapa et al. 2006), strategies for the assessment of MAS can be determined. These strategies will likely incorporate the use of both MAS and conventional breeding for designing an optimal approach for increasing yield in melon.

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